

STIC Biotechnology Systems Branch

RAW SEQUENCE LISTING **ERROR REPORT**

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/533,299
Source: pc
Date Processed by STIC: 6/30/06

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER VERSION 4.4.0 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):
U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/10/06

Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER: 10/533,299

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics
 Wrapped Aminos The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor **after** creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2 ✓ Invalid Line Length The rules require that a line **not exceed** 72 characters in length. This includes white spaces.
- 3 Misaligned Amino
 Numbering The numbering under each 5th amino acid is misaligned. Do **not** use tab codes between numbers; use **space characters**, instead.
- 4 ✓ Non-ASCII The submitted file was **not** saved in ASCII(DOS) text, as **required** by the Sequence Rules. **Please ensure your subsequent submission is saved in ASCII text.**
- 5 Variable Length Sequence(s) contain n's or Xaa's representing more than one residue. **Per Sequence Rules, each n or Xaa can only represent a single residue.** Please present the **maximum** number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 PatentIn 2.0
 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. **This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.**
- 7 Skipped Sequences
 (OLD RULES) Sequence(s) missing. If intentional, please insert the following lines for **each** skipped sequence:
 (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
 (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 This sequence is intentionally skipped
 Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to **include** the skipped sequences.
- 8 Skipped Sequences
 (NEW RULES) Sequence(s) missing. If **intentional**, please insert the following lines for **each** skipped sequence.
 <210> sequence id number
 <400> sequence id number
 000
- 9 Use of n's or Xaa's
 (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
 Per 1.823 of Sequence Rules, use of <220>-<223> is **MANDATORY** if n's or Xaa's are present.
 In <220> to <223> section, please explain location of **n** or **Xaa**, and which residue **n** or **Xaa** represents.
- 10 Invalid <213>
 Response Per 1.823 of Sequence Rules, the only **valid** <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is **required** when <213> response is Unknown or is Artificial Sequence. (see item 11 below)
- 11 ✓ Use of <220> Sequence(s) 13, 14, 15, 16, 17 missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is **MANDATORY** if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section or use "chemically synthesized" as explanation. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32), also Sec. 1.823 of Sequence Rules
- 12 PatentIn 2.0
 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13 Misuse of n/Xaa "n" can **only** represent a single nucleotide; "Xaa" can **only** represent a single amino acid



PCT

RAW SEQUENCE LISTING

DATE: 06/30/2006

PATENT APPLICATION: US/10/533,299

TIME: 08:27:09

Input Set : A:\PTO.RJ.txt

Output Set: N:\CRF4\06302006\J533299.raw

4 <110> APPLICANT: Pieris Proteolab AG
 6 <120> TITLE OF INVENTION: Soluble truncated polypeptides of the Nogo-A protein,
 methods for the
 7 production of such polypeptides and methods for identifying compounds having
 8 detectable affinity to a Nogo-A protein
 C--> 10 <140> CURRENT APPLICATION NUMBER: US/10/533,299
 C--> 10 <141> CURRENT FILING DATE: 2005-04-29
 W--> 0 <130> FILE REFERENCE:
 E--> 10 <160> NUMBER OF SEQ ID NOS: 18

see item 4 on Enor summary sheet; also, see item 2 on Enor summary sheet

17 (see p. 12)

ERRORED SEQUENCES

12 <210> SEQ ID NO: 1
 13 <211> LENGTH: 1163
 14 <212> TYPE: PRT
 15 <213> ORGANISM: Rattus norvegicus
 17 <220> FEATURE:
 18 <223> OTHER INFORMATION: rat Nogo-A protein
 20 <400> SEQUENCE: 1

22	Met	Glu	Asp	Ile	Asp	Gln	Ser	Ser	Leu	Val	Ser	Ser	Ser	Thr	Asp
23	1				5					10					15
25	Ser	Pro	Pro	Arg	Pro	Pro	Pro	Ala	Phe	Lys	Tyr	Gln	Phe	Val	Thr
26					20					25					30
28	Glu	Pro	Glu	Asp	Glu	Glu	Asp	Glu	Glu	Glu	Glu	Glu	Asp	Glu	Glu
29					35					40					45
31	Glu	Asp	Asp	Glu	Asp	Leu	Glu	Glu	Leu	Glu	Val	Leu	Glu	Arg	Lys
32					50					55					60
34	Pro	Ala	Ala	Gly	Leu	Ser	Ala	Ala	Ala	Val	Pro	Pro	Ala	Ala	Ala
35					65					70					75
37	Ala	Pro	Leu	Leu	Asp	Phe	Ser	Ser	Asp	Ser	Val	Pro	Pro	Ala	Pro
38					80					85					90
40	Arg	Gly	Pro	Leu	Pro	Ala	Ala	Pro	Pro	Ala	Ala	Pro	Glu	Arg	Gln
41					95					100					105
43	Pro	Ser	Trp	Glu	Arg	Ser	Pro	Ala	Ala	Pro	Ala	Pro	Ser	Leu	Pro
44					110					115					120
46	Pro	Ala	Ala	Ala	Val	Leu	Pro	Ser	Lys	Leu	Pro	Glu	Asp	Asp	Glu
47					125					130					135
49	Pro	Pro	Ala	Arg	Pro	Pro	Pro	Pro	Pro	Pro	Ala	Gly	Ala	Ser	Pro
50					140					145					150
52	Leu	Ala	Glu	Pro	Ala	Ala	Pro	Pro	Ser	Thr	Pro	Ala	Ala	Pro	Lys
53					155					160					165
55	Arg	Arg	Gly	Ser	Gly	Ser	Val	Asp	Glu	Thr	Leu	Phe	Ala	Leu	Pro
56					170					175					180

see p. 21

**Does Not Comply
Corrected Diskette Needed**

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DATE: 06/30/2006

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Input Set : A:\PTO.RJ.txt

Output Set: N:\CRF4\06302006\J533299.raw

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58 Ala Ala Ser Glu Pro Val Ile Pro Ser Ser Ala Glu Lys Ile Met
59                      185                      190                      195
61 Asp Leu Met Glu Gln Pro Gly Asn Thr Val Ser Ser Gly Gln Glu
62                      200                      205                      210
64 Asp Phe Pro Ser Val Leu Leu Glu Thr Ala Ala Ser Leu Pro Ser
65                      215                      220                      225
67 Leu Ser Pro Leu Ser Thr Val Ser Phe Lys Glu His Gly Tyr Leu
68                      230                      235                      240
70 Gly Asn Leu Ser Ala Val Ser Ser Ser Glu Gly Thr Ile Glu Glu
71                      245                      250                      255
73 Thr Leu Asn Glu Ala Ser Lys Glu Leu Pro Glu Arg Ala Thr Asn
74                      260                      265                      270
76 Pro Phe Val Asn Arg Asp Leu Ala Glu Phe Ser Glu Leu Glu Tyr
77                      275                      280                      285
79 Ser Glu Met Gly Ser Ser Phe Lys Gly Ser Pro Lys Gly Glu Ser
E--> 80          290          295          310 300
82 Ala Ile Leu Val Glu Asn Thr Lys Glu Glu Val Ile Val Arg Ser
83                      305                      310                      315
85 Lys Asp Lys Glu Asp Leu Val Cys Ser Ala Ala Leu His Ser Pro
86                      320                      325                      330
88 Gln Glu Ser Pro Val Gly Lys Glu Asp Arg Val Val Ser Pro Glu
89                      335                      340                      345
91 Lys Thr Met Asp Ile Phe Asn Glu Met Gln Met Ser Val Val Ala
92                      350                      355                      360
94 Pro Val Arg Glu Glu Tyr Ala Asp Phe Lys Pro Phe Glu Gln Ala
95                      365                      370                      375
97 Trp Glu Val Lys Asp Thr Tyr Glu Gly Ser Arg Asp Val Leu Ala
98                      380                      385                      390
100 Ala Arg Ala Asn Val Glu Ser Lys Val Asp Arg Lys Cys Leu Glu
101                      395                      400                      405
103 Asp Ser Leu Glu Gln Lys Ser Leu Gly Lys Asp Ser Glu Gly Arg
104                      410                      415                      420
106 Asn Glu Asp Ala Ser Phe Pro Ser Thr Pro Glu Pro Val Lys Asp
107                      425                      430                      435
109 Ser Ser Arg Ala Tyr Ile Thr Cys Ala Ser Phe Thr Ser Ala Thr
110                      440                      445                      450
112 Glu Ser Thr Thr Ala Asn Thr Phe Pro Leu Leu Glu Asp His Thr
113                      455                      460                      465
115 Ser Glu Asn Lys Thr Asp Glu Lys Lys Ile Glu Glu Arg Lys Ala
116                      470                      475                      480
118 Gln Ile Ile Thr Glu Lys Thr Ser Pro Lys Thr Ser Asn Pro Phe
119                      485                      490                      495
121 Leu Val Ala Val Gln Asp Ser Glu Ala Asp Tyr Val Thr Thr Asp
122                      500                      505                      510
124 Thr Leu Ser Lys Val Thr Glu Ala Ala Val Ser Asn Met Pro Glu
125                      515                      520                      525
127 Gly Leu Thr Pro Asp Leu Val Gln Glu Ala Cys Glu Ser Glu Leu
128                      530                      535                      540
130 Asn Glu Ala Thr Gly Thr Lys Ile Ala Tyr Glu Thr Lys Val Asp

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Input Set : A:\PTO.RJ.txt

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131		545		550		555
133	Leu Val Gln Thr	Ser Glu Ala Ile Gln	Glu Ser Leu Tyr Pro	Thr		
134		560		565		570
136	Ala Gln Leu Cys	Pro Ser Phe Glu Glu	Ala Glu Ala Thr Pro	Ser		
137		575		580		585
139	Pro Val Leu Pro	Asp Ile Val Met Glu	Ala Pro Leu Asn Ser	Leu		
140		590		595		600
142	Leu Pro Ser Ala	Gly Ala Ser Val Val	Gln Pro Ser Val Ser	Pro		
143		605		610		615
145	Leu Glu Ala Pro	Pro Pro Val Ser Tyr	Asp Ser Ile Lys Leu	Glu		
146		620		625		630
148	Pro Glu Asn Pro	Pro Pro Tyr Glu Glu	Ala Met Asn Val Ala	Leu		
149		635		640		645
151	Lys Ala Leu Gly	Thr Lys Glu Gly Ile	Lys Glu Pro Glu Ser	Phe		
152		650		655		660
154	Asn Ala Ala Val	Gln Glu Thr Glu Ala	Pro Tyr Ile Ser Ile	Ala		
155		665		670		675
157	Cys Asp Leu Ile	Lys Glu Thr Lys Leu	Ser Thr Glu Pro Ser	Pro		
158		680		685		690
160	Asp Phe Ser Asn	Tyr Ser Glu Ile Ala	Lys Phe Glu Lys Ser	Val		
161		695		700		705
163	Pro Glu His Ala	Glu Leu Val Glu Asp	Ser Ser Pro Glu Ser	Glu		
164		710		715		720
166	Pro Val Asp Leu	Phe Ser Asp Asp Ser	Ile Pro Glu Val Pro	Gln		
167		725		730		735
169	Thr Gln Glu Glu	Ala Val Met Leu Met	Lys Glu Ser Leu Thr	Glu		
170		740		745		750
172	Val Ser Glu Thr	Val Ala Gln His Lys	Glu Glu Arg Leu Ser	Ala		
173		755		760		765
175	Ser Pro Gln Glu	Leu Gly Lys Pro Tyr	Leu Glu Ser Phe Gln	Pro		
176		770		775		780
178	Asn Leu His Ser	Thr Lys Asp Ala Ala	Ser Asn Asp Ile Pro	Thr		
179		785		790		795
181	Leu Thr Lys Lys	Glu Lys Ile Ser Leu	Gln Met Glu Glu Phe	Asn		
182		800		805		810
184	Thr Ala Ile Tyr	Ser Asn Asp Asp Leu	Leu Ser Ser Lys Glu	Asp		
185		815		820		825
187	Lys Ile Lys Glu	Ser Glu Thr Phe Ser	Asp Ser Ser Pro Ile	Glu		
188		830		835		840
190	Ile Ile Asp Glu	Phe Pro Thr Phe Val	Ser Ala Lys Asp Asp	Ser		
191		845		850		855
193	Pro Lys Leu Ala	Lys Glu Tyr Thr Asp	Leu Glu Val Ser Asp	Lys		
194		860		865		870
196	Ser Glu Ile Ala	Asn Ile Gln Ser Gly	Ala Asp Ser Leu Pro	Cys		
197		875		880		885
199	Leu Glu Leu Pro	Cys Asp Leu Ser Phe	Lys Asn Ile Tyr Pro	Lys		
200		890		895		900
202	Asp Glu Val His	Val Ser Asp Glu Phe	Ser Glu Asn Arg Ser	Ser		
203		905		910		915

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205 Val Ser Lys Ala Ser Ile Ser Pro Ser Asn Val Ser Ala Leu Glu
 206 920 925 930
 208 Pro Gln Thr Glu Met Gly Ser Ile Val Lys Ser Lys Ser Leu Thr
 209 935 940 945
 211 Lys Glu Ala Glu Lys Lys Leu Pro Ser Asp Thr Glu Lys Glu Asp
 212 950 955 960
 214 Arg Ser Leu Ser Ala Val Leu Ser Ala Glu Leu Ser Lys Thr Ser
 215 965 970 975
 217 Val Val Asp Leu Leu Tyr Trp Arg Asp Ile Lys Lys Thr Gly Val
 218 980 985 990
 220 Val Phe Gly Ala Ser Leu Phe Leu Leu Leu Ser Leu Thr Val Phe
 221 995 1000 1005
 223 Ser Ile Val Ser Val Thr Ala Tyr Ile Ala Leu Ala Leu Leu Ser
 224 1010 1015 1020
 226 Val Thr Ile Ser Phe Arg Ile Tyr Lys Gly Val Ile Gln Ala Ile
 E--> 227 1030/1025 1030 1035
 229 Gln Lys Ser Asp Glu Gly His Pro Phe Arg Ala Tyr Leu Glu Ser
 230 1040 1045 1050
 232 Glu Val Ala Ile Ser Glu Glu Leu Val Gln Lys Tyr Ser Asn Ser
 233 1055 1060 1065
 235 Ala Leu Gly His Val Asn Ser Thr Ile Lys Glu Leu Arg Arg Leu
 236 1070 1075 1080
 238 Phe Leu Val Asp Asp Leu Val Asp Ser Leu Lys Phe Ala Val Leu
 239 1085 1090 1095
 241 Met Trp Val Phe Thr Tyr Val Gly Ala Leu Phe Asn Gly Leu Thr
 242 1100 1105 1110
 244 Leu Leu Ile Leu Ala Leu Ile Ser Leu Phe Ser Ile Pro Val Ile
 245 1115 1120 1125
 247 Tyr Glu Arg His Gln Val Gln Ile Asp His Tyr Leu Gly Leu Ala
 248 1130 1135 1140
 250 Asn Lys Ser Val Lys Asp Ala Met Ala Lys Ile Gln Ala Lys Ile
 E--> 251 1145 1150 1155
 253 Pro Gly Leu Lys Arg Lys Ala Asp
 OK-> 254 1160
 258 <210> SEQ ID NO: 2
 259 <211> LENGTH: 1192
 260 <212> TYPE: PRT
 261 <213> ORGANISM: Homo sapiens
 263 <220> FEATURE:
 264 <223> OTHER INFORMATION: human Nogo-A protein
 266 <400> SEQUENCE: 2
 268 Met Glu Asp Leu Asp Gln Ser Pro Leu Val Ser Ser Ser Asp Ser
 269 1 5 10 15
 271 Pro Pro Arg Pro Gln Pro Ala Phe Arg Tyr Gln Phe Val Arg Glu
 272 20 25 30
 274 Pro Glu Asp Glu Glu Glu Glu Glu Glu Glu Glu Asp Glu
 275 35 40 45
 277 Asp Glu Asp Leu Glu Glu Leu Glu Val Leu Glu Arg Lys Pro Ala
 278 50 55 60

see
p. 5

move numbers
 directly under
 first letter of
 the amino
 acid

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Output Set: N:\CRF4\06302006\J533299.raw

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280 Ala Gly Leu Ser Ala Ala Pro Val Pro Thr Ala Pro Ala Ala Gly
281          65          70          75
283 Ala Pro Leu Met Asp Phe Gly Asn Glu Phe Val Pro Pro Ala Pro
284          80          85          90
286 Arg Gly Pro Leu Pro Ala Ala Pro Pro Val Ala Pro Glu Arg Gln
287          95          100         105
289 Pro Ser Trp Asp Pro Ser Pro Val Ser Ser Thr Val Pro Ala Pro
290         110         115         120
292 Ser Pro Leu Ser Ala Ala Ala Val Ser Pro Ser Lys Leu Pro Glu
293         125         130         135
295 Asp Asp Glu Pro Pro Ala Arg Pro Pro Pro Pro Pro Ala Ser
296         140         145         150
298 Val Ser Pro Gln Ala Glu Pro Val Trp Thr Pro Pro Ala Pro Ala
299         155         160         165
301 Pro Ala Ala Pro Pro Ser Thr Pro Ala Ala Pro Lys Arg Arg Gly
302         170         175         180
304 Ser Ser Gly Ser Val Asp Glu Thr Leu Phe Ala Leu Pro Ala Ala
305         185         190         195
307 Ser Glu Pro Val Ile Arg Ser Ser Ala Glu Asn Met Glu Leu Lys
308         200         205         210
310 Glu Gln Pro Gly Asn Thr Ile Ser Ala Gly Gln Glu Asp Phe Pro
311         215         220         225
313 Ser Val Leu Leu Glu Thr Ala Ala Ser Leu Pro Ser Leu Ser Pro
314         230         235         240
316 Leu Ser Ala Ala Ser Phe Lys Glu His Glu Tyr Leu Glu Asn Leu
317         245         250         255
319 Ser Thr Val Leu Pro Thr Glu Gly Thr Leu Gln Glu Asn Val Ser
320         260         265         270
322 Glu Ala Ser Lys Glu Val Ser Glu Lys Ala Lys Thr Leu Leu Ile
323         275         280         285
325 Asp Arg Asp Leu Thr Glu Phe Ser Glu Leu Glu Tyr Ser Glu Met
326         290         295         300
328 Gly Ser Ser Phe Ser Val Ser Pro Lys Ala Glu Ser Ala Val Ile
329         305         310         315
331 Val Ala Asn Pro Arg Glu Glu Ile Ile Val Lys Asn Lys Asp Glu
332         320         325         330
334 Glu Glu Lys Leu Val Ser Asn Asn Ile Leu His Asn Gln Gln Glu
335         335         340         345
337 Leu Pro Thr Ala Leu Thr Lys Leu Val Lys Glu Asp Glu Val Val
338         350         355         360
340 Ser Ser Glu Lys Ala Lys Asp Ser Phe Asn Glu Lys Arg Val Ala
E--> 341         365         370         385 375
343 Val Glu Ala Pro Met Arg Glu Glu Tyr Ala Asp Phe Lys Pro Phe
344         380         385         390
346 Glu Arg Val Trp Glu Val Lys Asp Ser Lys Glu Asp Ser Asp Met
347         395         400         405
349 Leu Ala Ala Gly Gly Lys Ile Glu Ser Asn Leu Glu Ser Lys Val
350         410         415         420
352 Asp Lys Lys Cys Phe Ala Asp Ser Leu Glu Gln Thr Asn His Glu

```

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Input Set : A:\PTO.RJ.txt

Output Set: N:\CRF4\06302006\J533299.raw

353		425		430		435
355	Lys Asn Ser Glu Ser Ser Asn Asp Asp Thr Ser Phe Pro Ser Thr					
356		440		445		450
358	Pro Glu Gly Ile Lys Asp Arg Pro Gly Ala Tyr Ile Thr Cys Ala					
359		455		460		465
361	Pro Phe Asn Pro Ala Ala Thr Glu Ser Ile Ala Thr Asn Ile Phe					
362		470		475		480
364	Pro Leu Leu Gly Asp Pro Thr Ser Glu Asn Lys Thr Asp Glu Lys					
365		485		490		495
367	Lys Ile Glu Glu Lys Lys Ala Gln Ile Val Thr Glu Lys Asn Thr					
368		500		505		510
370	Ser Thr Lys Thr Ser Asn Pro Phe Leu Val Ala Ala Gln Glu Ser					
371		515		520		525
373	Glu Thr Asp Tyr Val Thr Thr Asp Asn Leu Thr Lys Val Thr Glu					
374		530		535		540
376	Glu Val Val Ala Asn Met Pro Glu Gly Leu Thr Pro Asp Leu Val					
377		545		550		555
379	Gln Glu Ala Cys Glu Ser Glu Leu Asn Glu Val Thr Gly Thr Lys					
380		560		565		570
382	Ile Ala Tyr Glu Thr Lys Met Asp Leu Val Gln Thr Ser Glu Val					
383		575		580		585
385	Met Gln Glu Ser Leu Tyr Pro Ala Ala Gln Leu Cys Pro Ser Phe					
386		590		595		600
388	Glu Glu Ser Glu Ala Thr Pro Ser Pro Val Leu Pro Asp Ile Val					
389		605		610		615
391	Met Glu Ala Pro Leu Asn Ser Ala Val Pro Ser Ala Gly Ala Ser					
392		620		625		630
394	Val Ile Gln Pro Ser Ser Ser Pro Leu Glu Ala Ser Ser Val Gln					
395		635		640		645
397	Tyr Glu Ser Ile Lys His Glu Pro Glu Asn Pro Pro Pro Tyr Glu					
398		650		655		660
400	Glu Ala Met Ser Val Ser Leu Lys Lys Val Ser Gly Ile Lys Glu					
401		665		670		675
403	Glu Ile Lys Glu Pro Glu Asn Ile Asn Ala Ala Leu Gln Glu Thr					
404		680		685		690
406	Glu Ala Pro Tyr Ile Ser Ile Ala Cys Asp Leu Ile Lys Glu Thr					
407		695		700		705
409	Lys Leu Ser Ala Glu Pro Ala Pro Glu Phe Ser Asp Tyr Ser Glu					
410		710		715		720
412	Met Ala Lys Val Glu Gln Pro Val Pro Asp His Ser Glu Leu Val					
413		725		730		735
415	Glu Asp Ser Ser Pro Asp Ser Glu Pro Val Asp Leu Phe Ser Asp					
416		740		745		750
418	Asp Ser Ile Pro Asp Val Pro Gln Lys Gln Asp Glu Thr Val Met					
419		755		760		765
421	Leu Val Lys Glu Ser Leu Thr Glu Thr Ser Phe Glu Ser Met Ile					
422		770		775		780
424	Glu Tyr Glu Gln Lys Glu Lys Leu Ser Ala Leu Pro Pro Glu Gly					
425		785		790		795

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Input Set : A:\PTO.RJ.txt

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427	Gly	Lys	Pro	Tyr	Leu	Glu	Ser	Phe	Lys	Leu	Ser	Leu	Asp	Asn	Thr
428					800					805					810
430	Lys	Asp	Thr	Leu	Leu	Pro	Asp	Glu	Val	Ser	Thr	Leu	Ser	Lys	Lys
431					815					820					825
433	Glu	Lys	Ile	Pro	Ile	Gln	Met	Glu	Glu	Leu	Ser	Thr	Ala	Val	Tyr
434					830					835					840
436	Ser	Asn	Asp	Asp	Leu	Phe	Ile	Ser	Lys	Glu	Ala	Gln	Ile	Arg	Glu
437					845					850					855
439	Thr	Glu	Thr	Phe	Ser	Asp	Ser	Ser	Pro	Ile	Glu	Ile	Ile	Asp	Glu
440					860					865					870
442	Phe	Pro	Thr	Leu	Ile	Ser	Ser	Lys	Thr	Asp	Ser	Phe	Ser	Lys	Leu
443					875					880					885
445	Ala	Arg	Glu	Tyr	Thr	Asp	Leu	Glu	Val	Ser	His	Lys	Ser	Glu	Ile
446					890					895					900
448	Ala	Gln	Ala	Pro	Asp	Gly	Ala	Gly	Ser	Leu	Pro	Cys	Thr	Glu	Leu
449					905					910					915
451	Pro	His	Asp	Leu	Ser	Leu	Lys	Asn	Ile	Gln	Pro	Lys	Val	Glu	Glu
452					920					925					930
454	Lys	Ile	Ser	Phe	Ser	Asp	Asp	Phe	Ser	Lys	Asn	Gly	Ser	Ala	Thr
455					935					940					945
457	Ser	Lys	Val	Leu	Leu	Leu	Pro	Pro	Asp	Val	Ser	Ala	Leu	Ala	Thr
458					950					955					960
460	Gln	Ala	Glu	Ile	Glu	Ser	Ile	Val	Lys	Pro	Lys	Val	Leu	Val	Lys
461					965					970					975
463	Glu	Ala	Glu	Lys	Lys	Leu	Pro	Ser	Asp	Thr	Glu	Lys	Glu	Asp	Arg
464					980					985					990
466	Ser	Pro	Ser	Ala	Ile	Phe	Ser	Ala	Glu	Leu	Ser	Lys	Thr	Ser	Val
467					995					1000					1005
469	Val	Asp	Leu	Leu	Tyr	Trp	Arg	Asp	Ile	Lys	Lys	Thr	Gly	Val	Val
470					1010					1015					1020
472	Phe	Gly	Ala	Ser	Leu	Phe	Leu	Leu	Leu	Ser	Leu	Thr	Val	Phe	Ser
473					1025					1030					1035
475	Ile	Val	Ser	Val	Thr	Ala	Tyr	Ile	Ala	Leu	Ala	Leu	Leu	Ser	Val
476					1040					1045					1050
478	Thr	Ile	Ser	Phe	Arg	Ile	Tyr	Lys	Gly	Val	Ile	Gln	Ala	Ile	Gln
479					1055					1060					1065
481	Lys	Ser	Asp	Glu	Gly	His	Pro	Phe	Arg	Ala	Tyr	Leu	Glu	Ser	Glu
482					1070					1075					1080
484	Val	Ala	Ile	Ser	Glu	Glu	Leu	Val	Gln	Lys	Tyr	Ser	Asn	Ser	Ala
485					1085					1090					1095
487	Leu	Gly	His	Val	Asn	Cys	Thr	Ile	Lys	Glu	Leu	Arg	Arg	Leu	Phe
488					1100					1105					1110
490	Leu	Val	Asp	Asp	Leu	Val	Asp	Ser	Leu	Lys	Phe	Ala	Val	Leu	Met
491					1115					1120					1125
493	Trp	Val	Phe	Thr	Tyr	Val	Gly	Ala	Leu	Phe	Asn	Gly	Leu	Thr	Leu
494					1130					1135					1140
496	Leu	Ile	Leu	Ala	Leu	Ile	Ser	Leu	Phe	Ser	Val	Pro	Val	Ile	Tyr
497					1145					1150					1155
499	Glu	Arg	His	Gln	Ala	Gln	Ile	Asp	His	Tyr	Leu	Gly	Leu	Ala	Asn

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500 1160 1165 1170
 502 Lys Asn Val Lys Asp Ala Met Ala Lys Ile Gln Ala Lys Ile Pro
 503 1175 1180 1185
 505 Gly Leu Lys Arg Lys Ala Glu
 506 1190
 723 <210> SEQ ID NO: 13
 724 <211> LENGTH: 2248
 725 <212> TYPE: DNA
 726 <213> ORGANISM: Artificial sequence
 728 <220> FEATURE:
 729 <221> NAME/KEY: sig_peptide
 730 <222> LOCATION: (22)...(84)
 732 <220> FEATURE:
 733 <221> NAME/KEY: mat_peptide
 734 <222> LOCATION: (85)...(2238)
 735 <223> OTHER INFORMATION: fusion protein of truncated rat Nogo-A fragment and Strep-tag II

*(the entire sequence)
 this needs explanation in
 2207-2237 section
 see p. 11, too
 (see item 11 on Euro summary
 sheet) same error in seq. 14,
 15, 16, 17*

737 <220> FEATURE:
 738 <221> NAME/KEY: CDS
 739 <222> LOCATION: (85)...(2208)
 740 <223> OTHER INFORMATION: mature truncated Nogo-A
 742 <220> FEATURE:
 743 <221> NAME/KEY: CDS
 744 <222> LOCATION: (2209)...(2238)
 745 <223> OTHER INFORMATION: Strep-tag II affinity tag
 748 <400> SEQUENCE: 13

752 tctagataac gagggcaaaa a atg aaa aag aca gct atc gcg att 45
 753 Met Lys Lys Thr Ala Ile Ala Ile
 754 -21 -20 -15
 756 gca gtg gca ctg gct ggt ttc gct acc gta gcg cag gcc tct ttt 90
 757 Ala Val Ala Leu Ala Gly Phe Ala Thr Val Ala Gln Ala Ser Phe
 758 -10 -5 -1 1
 760 aaa gaa cat gga tac ctt ggt aac tta tca gca gtg tca tcc tca 135
 761 Lys Glu His Gly Tyr Leu Gly Asn Leu Ser Ala Val Ser Ser Ser
 762 5 10 15
 764 gaa gga aca att gaa gaa act tta aat gaa gct tct aaa gag ttg 180
 765 Glu Gly Thr Ile Glu Glu Thr Leu Asn Glu Ala Ser Lys Glu Leu
 766 20 25 30
 768 cca gag agg gca aca aat cca ttt gta aat aga gat tta gca gaa 225
 769 Pro Glu Arg Ala Thr Asn Pro Phe Val Asn Arg Asp Leu Ala Glu
 770 35 40 45
 772 ttt tca gaa tta gaa tat tca gaa atg gga tca tct ttt aaa ggc 270
 773 Phe Ser Glu Leu Glu Tyr Ser Glu Met Gly Ser Ser Phe Lys Gly
 774 50 55 60
 776 tcc cca aaa gga gag tca gcc ata tta gta gaa aac act aag gaa 315
 777 Ser Pro Lys Gly Glu Ser Ala Ile Leu Val Glu Asn Thr Lys Glu
 778 65 70 75
 780 gaa gta att gtg agg agt aaa gac aaa gag gat tta gtt tgt agt 360
 781 Glu Val Ile Val Arg Ser Lys Asp Lys Glu Asp Leu Val Cys Ser
 782 80 85 90

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```

784 gca gcc ctt cac agt cca caa gaa tca cct gtg ggt aaa gaa gac 405
785 Ala Ala Leu His Ser Pro Gln Glu Ser Pro Val Gly Lys Glu Asp
786      95      100      105
788 aga gtt gtg tct cca gaa aag aca atg gac att ttt aat gaa atg 450
789 Arg Val Val Ser Pro Glu Lys Thr Met Asp Ile Phe Asn Glu Met
790      110      115      120
792 cag atg tca gta gta gca cct gtg agg gaa gag tat gca gac ttt 495
793 Gln Met Ser Val Val Ala Pro Val Arg Glu Glu Tyr Ala Asp Phe
794      125      130      135
796 aag cca ttt gaa caa gca tgg gaa gtg aaa gat act tat gag gga 540
797 Lys Pro Phe Glu Gln Ala Trp Glu Val Lys Asp Thr Tyr Glu Gly
798      140      145      150
800 agt agg gat gtg ctg gct gct aga gct aat gtg gaa agt aaa gtg 585
801 Ser Arg Asp Val Leu Ala Ala Arg Ala Asn Val Glu Ser Lys Val
802      155      160      165
804 gac aga aaa tgc ttg gaa gat agc ctg gag caa aaa agt ctt ggg 630
805 Asp Arg Lys Cys Leu Glu Asp Ser Leu Glu Gln Lys Ser Leu Gly
806      170      175      180
808 aag gat agt gaa ggc aga aat gag gat gct tct ttc ccc agt acc 675
809 Lys Asp Ser Glu Gly Arg Asn Glu Asp Ala Ser Phe Pro Ser Thr
810      185      190      195
812 cca gaa cct gtg aag gac agc tcc aga gca tat att acc tgt gct 720
813 Pro Glu Pro Val Lys Asp Ser Ser Arg Ala Tyr Ile Thr Cys Ala
814      200      205      210
816 tcc ttt acc tca gca acc gaa agc acc aca gca aac act ttc cct 765
817 Ser Phe Thr Ser Ala Thr Glu Ser Thr Thr Ala Asn Thr Phe Pro
818      215      220      225
820 ttg tta gaa gat cat act tca gaa aat aaa aca gat gaa aaa aaa 810
821 Leu Leu Glu Asp His Thr Ser Glu Asn Lys Thr Asp Glu Lys Lys
822      230      235      240
824 ata gaa gaa agg aag gcc caa att ata aca gag aag act agc ccc 855
825 Ile Glu Glu Arg Lys Ala Gln Ile Ile Thr Glu Lys Thr Ser Pro
826      245      250      255
828 aaa acg tca aat cct ttc ctt gta gca gta cag gat tct gag gca 900
829 Lys Thr Ser Asn Pro Phe Leu Val Ala Val Gln Asp Ser Glu Ala
830      260      265      270
832 gat tat gtt aca aca gat acc tta tca aag gtg act gag gca gca 945
833 Asp Tyr Val Thr Thr Asp Thr Leu Ser Lys Val Thr Glu Ala Ala
834      275      280      285
836 gtg tca aac atg cct gaa ggt ctg acg cca gat tta gtt cag gaa 990
837 Val Ser Asn Met Pro Glu Gly Leu Thr Pro Asp Leu Val Gln Glu
838      290      295      300
840 gca tgt gaa agt gaa ctg aat gaa gcc aca ggt aca aag att gct 1035
841 Ala Cys Glu Ser Glu Leu Asn Glu Ala Thr Gly Thr Lys Ile Ala
842      305      310      315
844 tat gaa aca aaa gtg gac ttg gtc caa aca tca gaa gct ata caa 1080
845 Tyr Glu Thr Lys Val Asp Leu Val Gln Thr Ser Glu Ala Ile Gln
846      320      325      330
848 gaa tca ctt tac ccc aca gca cag ctt tgc cca tca ttt gag gaa 1125

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Input Set : A:\PTO.RJ.txt

Output Set: N:\CRF4\06302006\J533299.raw

```

849 Glu Ser Leu Tyr Pro Thr Ala Gln Leu Cys Pro Ser Phe Glu Glu
850      335      340      345
852 gct gaa gca act ccg tca cca gtt ttg cct gat att gtt atg gaa 1170
853 Ala Glu Ala Thr Pro Ser Pro Val Leu Pro Asp Ile Val Met Glu
854      350      355      360
856 gca cca tta aat tct ctg ctt cca agc gct ggt gct tct gta gtg 1215
857 Ala Pro Leu Asn Ser Leu Leu Pro Ser Ala Gly Ala Ser Val Val
858      365      370      375
860 cag ccc agt gta tcc cca ctg gaa gca cct cct cca gtt agt tat 1260
861 Gln Pro Ser Val Ser Pro Leu Glu Ala Pro Pro Pro Val Ser Tyr
862      380      385      390
864 gac agt ata aag ctt gag cct gaa aac ccc cca cca tat gaa gaa 1305
865 Asp Ser Ile Lys Leu Glu Pro Glu Asn Pro Pro Pro Tyr Glu Glu
866      395      400      405
868 gcc atg aat gta gca cta aaa gct ttg gga aca aag gaa gga ata 1350
869 Ala Met Asn Val Ala Leu Lys Ala Leu Gly Thr Lys Glu Gly Ile
870      410      415      420
872 aaa gag cct gaa agt ttt aat gca gct gtt cag gaa aca gaa gct 1395
873 Lys Glu Pro Glu Ser Phe Asn Ala Ala Val Gln Glu Thr Glu Ala
874      425      430      435
876 cct tat ata tcc att gcg tgt gat tta att aaa gaa aca aag ctg 1440
877 Pro Tyr Ile Ser Ile Ala Cys Asp Leu Ile Lys Glu Thr Lys Leu
878      440      445      450
880 tcc act gag cca agt cca gat ttc tct aat tat tca gaa ata gca 1485
881 Ser Thr Glu Pro Ser Pro Asp Phe Ser Asn Tyr Ser Glu Ile Ala
882      455      460      465
884 aaa ttc gag aag tcg gtg ccc gaa cac gct gag cta gtg gag gat 1530
885 Lys Phe Glu Lys Ser Val Pro Glu His Ala Glu Leu Val Glu Asp
886      470      475      480
888 tcc tca cct gaa tct gaa cca gtt gac tta ttt agt gat gat tcg 1575
889 Ser Ser Pro Glu Ser Glu Pro Val Asp Leu Phe Ser Asp Asp Ser
890      485      490      495
892 att cct gaa gtc cca caa aca caa gag gag gct gtg atg ctg atg 1620
893 Ile Pro Glu Val Pro Gln Thr Gln Glu Glu Ala Val Met Leu Met
894      500      505      510
896 aag gag agt ctg act gaa gtg tct gag aca gta gcc cag cac aaa 1665
897 Lys Glu Ser Leu Thr Glu Val Ser Glu Thr Val Ala Gln His Lys
898      515      520      525
900 gag gag aga ctt agt gcc tca cct cag gag cta gga aag cca tat 1710
901 Glu Glu Arg Leu Ser Ala Ser Pro Gln Glu Leu Gly Lys Pro Tyr
902      530      535      540
904 tta gag tct ttt cag ccc aat tta cat agt aca aaa gat gct gca 1755
905 Leu Glu Ser Phe Gln Pro Asn Leu His Ser Thr Lys Asp Ala Ala
906      545      550      555
908 tct aat gac att cca aca ttg acc aaa aag gag aaa att tct ttg 1800
909 Ser Asn Asp Ile Pro Thr Leu Thr Lys Lys Glu Lys Ile Ser Leu
910      560      565      570
912 caa atg gaa gag ttt aat act gca att tat tca aat gat gac tta 1845
913 Gln Met Glu Glu Phe Asn Thr Ala Ile Tyr Ser Asn Asp Asp Leu

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914          575          580          585
916 ctt tct tct aag gaa gac aaa ata aaa gaa agt gaa aca ttt tca 1890
917 Leu Ser Ser Lys Glu Asp Lys Ile Lys Glu Ser Glu Thr Phe Ser
918          590          595          600
920 gat tca tct ccg att gag ata ata gat gaa ttt ccc acg ttt gtc 1935
921 Asp Ser Ser Pro Ile Glu Ile Ile Asp Glu Phe Pro Thr Phe Val
922          605          610          615
924 agt gct aaa gat gat tct cct aaa tta gcc aag gag tac act gat 1980
925 Ser Ala Lys Asp Asp Ser Pro Lys Leu Ala Lys Glu Tyr Thr Asp
926          620          625          630
928 cta gaa gta tcc gac aaa agt gaa att gct aat atc caa agc ggg 2025
929 Leu Glu Val Ser Asp Lys Ser Glu Ile Ala Asn Ile Gln Ser Gly
930          635          640          645
932 gca gat tca ttg cct tgc tta gaa ttg ccc tgt gac ctt tct ttc 2070
933 Ala Asp Ser Leu Pro Cys Leu Glu Leu Pro Cys Asp Leu Ser Phe
934          650          655          660
936 aag aat ata tat cct aaa gat gaa gta cat gtt tca gat gaa ttc 2115
937 Lys Asn Ile Tyr Pro Lys Asp Glu Val His Val Ser Asp Glu Phe
938          665          670          675
940 tcc gaa aat agg tcc agt gta tct aag gca tcc ata tcg cct tca 2160
941 Ser Glu Asn Arg Ser Ser Val Ser Lys Ala Ser Ile Ser Pro Ser
942          680          685          690
944 aat gtc tct gct ttg gaa cct cag aca gaa atg ggc agc ata gtt 2205
945 Asn Val Ser Ala Leu Glu Pro Gln Thr Glu Met Gly Ser Ile Val
946          695          700          705
948 aaa agc gct tgg cgt cac ccg cag ttc ggt ggt taa taa gctt 2248
E--> 949 Lys Ser Ala Trp Arg His Pro Gln Phe Gly Gly End delete - do not show anything
950          710          715
955 <210> SEQ ID NO: 14
956 <211> LENGTH: 2425
957 <212> TYPE: DNA
958 <213> ORGANISM: Artificial sequence
960 <220> FEATURE:
961 <221> NAME/KEY: sig_peptide
962 <222> LOCATION: (22)...(84)
964 <220> FEATURE:
965 <221> NAME/KEY: mat_peptide
966 <222> LOCATION: (85)..(2460)
967 <223> OTHER INFORMATION: fusion protein of truncated rat Nogo-A fragment and Strep-
tag II
969 <220> FEATURE:
970 <221> NAME/KEY: CDS
W--> 971 <222> LOCATION: (85)..(2430)
972 <223> OTHER INFORMATION: mature truncated Nogo-A
974 <220> FEATURE:
975 <221> NAME/KEY: CDS
W--> 976 <222> LOCATION: (2431)..(2460)
977 <223> OTHER INFORMATION: Strep-tag II affinity tag
980 <400> SEQUENCE: 14
983 tctagataac gagggcaaaa a atg aaa aag aca gct atc gcg att 45

```

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12

last sequence in submitted file

<210> 17

<211> 739

<212> PRT

<213> Artificial sequence

this needs explanation in 220-223 section

<220>

<221> SIGNAL

<222> (-21)...(-1)

<220>

<221> CHAIN

<222> (1)...(718)

<223> fusion protein of truncated rat Nogo-A fragment and Strep-tag II

<220>

<221>

<222> (1)...(708)

<223> mature truncated Nogo-A

<220>

<221>

<222> (709)...(718)

<223> Strep-tag affinity tag

<400> 17